

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:

Examiner #: _____ Date:

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Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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jan.delaval@uspto.gov

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Type of Search

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Searcher: awNA Sequence (#) 2

STN _____

Searcher Phone #: 4048

AA Sequence (#) _____

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Dr. Link _____

Date Completed: _____

Litigation _____

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Sequence Systems _____

Clerical Prep Time: 15

Patent Family _____

WWW/Internet _____

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605
Delaval, Jan

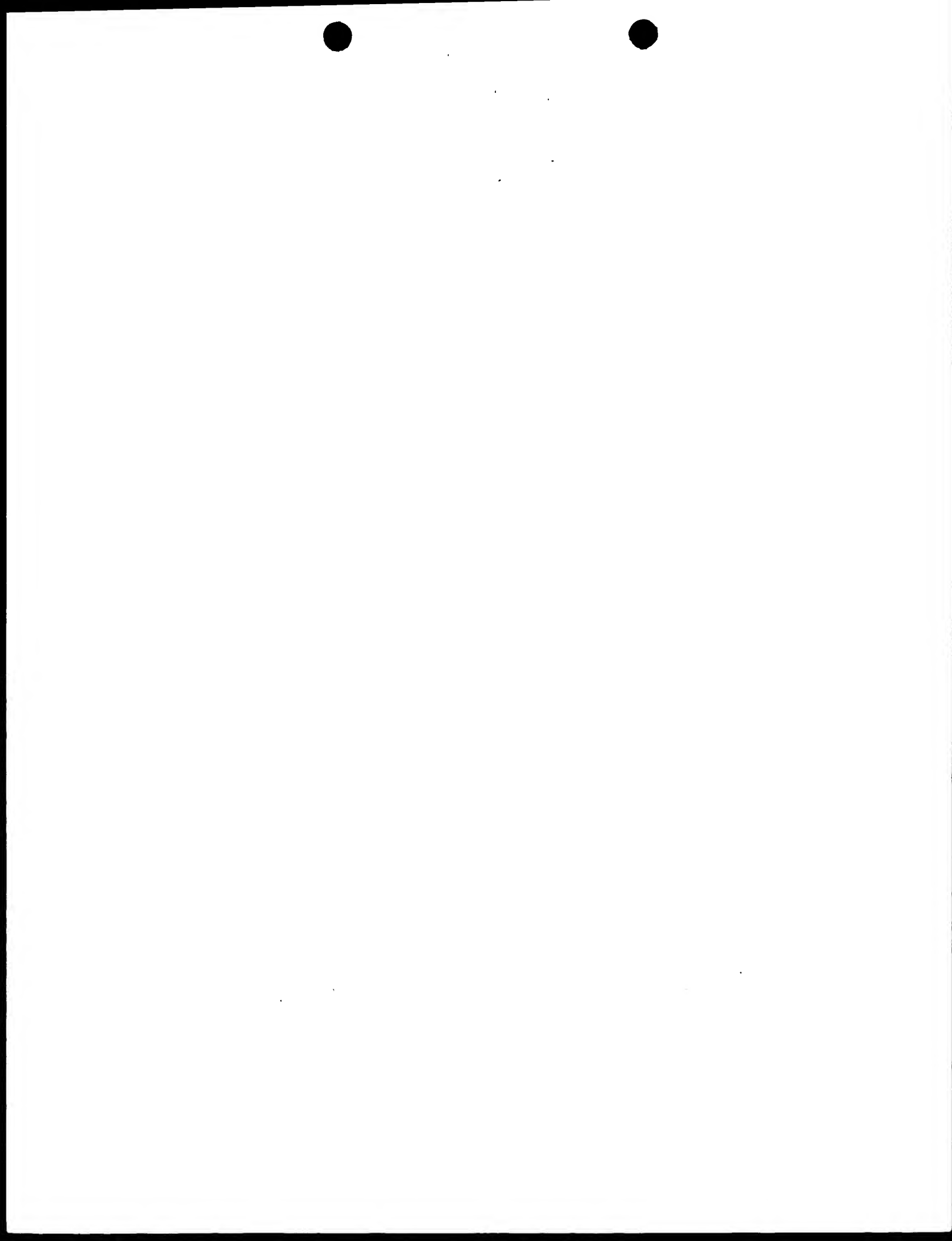
From: Jamroz, Margaret
Sent: Wednesday, February 13, 2002 10:27 AM
To: Delaval, Jan
Subject: 09/381,903

Jan,

Please do open search of SEQ ID NOS: 87, 88, 89, 90, 91, 92, and 93 of 09/381,903 with interference.

Thanks
Margaret (Megan) Jamroz
USPTO
AU 1644
Mailbox 9E12
CM1 9D04
(703) 308-8365

Jan Delaval
Reference Librarian
Biotechnology & Chemical Libr
CM1 1E07 - 703-308-4492
jan.delaval@uspto.gov



Revised version 4.5
(c) 1998 - 2000 CompuGen Ltd

Modeling and Simulation of a Parallel Distributed Processing Model

February 14, 2002. 14:28:54. Search time: 1.45 seconds
(with built-in compiler).
1.27.128 million ops. 1 updates/sec

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Series and color	Dimensions	Weight
Series 10000	100 mm x 100 mm	0.5

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End clock:	219.41 sops, 70.174552 resolutions	219.41

MAXIMUM	100	500	1000	5000	10000
100	100	100	100	100	100
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5000	100	500	1000	5000	5000
10000	100	500	1000	5000	10000

post	precession:	March 108
Maximum	March 108	
Minimum	first of summer	

[illegible]

total. N_{ij} is the number of results predicted by chain i in category j . N_{i+} is the number of results predicted by chain i in all categories. N_{+j} is the number of results in category j in all chains. N is the total number of results. \hat{p}_{ij} is the predicted probability of a result in category j by chain i . \hat{p}_{i+} is the predicted probability of a result in any category by chain i . \hat{p}_{+j} is the predicted probability of a result in category j . \hat{p}_{++} is the predicted probability of a result in any category. \hat{p}_{ij} and \hat{p}_{+j} are derived by analysis of the total score distribution.

SUMMARY

[illegible]

30	1.41	10.22	8.96	2	5.46, 4.26	clathrin assembly
41	1.41	10.22	9.15	2	8.64, 4.27	clathrin assembly
42	1.28, 5	10.0	4.60	2	7.8, 11.10	hypothetical protein
52	1.27	9.9	9.01	2	A4, 48.21	phosphoprotein, cy
53	1.27	9.9	4.21	2	1.00, 0.57	total protein, Esc
31	1.26	9.8	8.60	2	1.14, 6.50	total protein, Esc
45	1.26	9.8	9.78	2	1.14, 9.6	total protein, Esc
46	1.26	9.8	8.46	2	5.5, 4.1	phage lambda reat
47	1.25, 5	9.8	4.87	2	17.4, 4.97	GTP-binding reat
38	1.24, 5	9.7	4.09	2	3.8, 10.1	hypothetical protein
39	1.24	9.7	4.89	2	1.00, 6.3	polyhydroxy- α -keto
40	1.24	9.6	8.84	2	1.00, 6.3	polyhydroxy- α -keto
43	1.23	9.6	1.541	2	1.541	AAA protein, 14.171
42	1.22	9.5	2.17	2	8.29, 4.09	hypothetical protein
44	1.22	9.5	2.055	2	7.411, 1	extracellular matrix
44	1.21	9.4	3.94	2	E7, 0.596	probable PP1 protein
45	1.20, 5	9.4	8.01	2	1.2, 10.4	hypothetical protein

21-2121212121

RESULT 1
S48584
allergen Phl p Vb - common timothy
c:Species: Phleum pratense (common timothy)
c:Date: 06-Jan-1995 #sequence_revision: 06-Jan-1995 #text_change 08-Sep-1997
c:Accession: S48584
c:Author: A. Becker, W. Petersen, A. Schmitt, G. Stelzak, M.
Rehder, A. Ziegler, M. Biedermann, November 1994
submitted to the EMBL data library
Accession to the allergen Phl p Vb is highly homologous to a pathogenesis related
A:Reference number: S48584
A:Accession: S48584
A:Status: preliminary
A:Molecule type: mRNA
A:Accessions: 1-240 x 80%
A:Cross references: EMBL:Z27094; NID: 0114709; F03:0414710
c:Superfamily: grass pollen allergen 1x
c:Keywords: pollen

90, 98; See also 164; pp. 2; 1904th 280.

Woolly Ape		93-26;	Lt. L. No.	9707	
West Joral Stimulality					2; traps
Melches	247; conservative		mismatches	14;	tubols

[illegible]

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[illegible]

77. ИМПЛЕКЦИЈА ГИПЕРИВАЛСКИ АРОМАТИЗАНТИ И ПОСРЕДНИЦИ

QY	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	

[1] YUTYKOTSIJEAAVKQYAAIVAAATVOKYAVEFPAITKAIIMSEVYKVSQVNTIGAITV 2

196 YDYKCPSTLAAVKDAAATVAAAAL VNTAVFPAALIKATLALGVKVSQATLAAALV

241 AAGAAATTAAATGASGAATVAGGKYK = 60

1ab 256 AACAAATTAAGGASSTAAATTVAAGGGKVV 940

104449
altered V - velvet grass (loose) (104449)

Species: *Holotus lamarckii* (Verrill, 1881)
 Date: 20-Sep-1999 #sequence: 1
 Date: 20-Sep-1999 #text_change: 21
 Date: 20-Sep-1999 #total: 22

U. AVERSTROM, 1972, *Acta Path. Microbiol. Scand.*, **B78**, 1-12.
K. SCHRAMM, G. J. RULE, A. J. FORTINSON, A. J. SCHLACK, M. J. BOCKO, W. FORST, Biochem. 252, 200-206, 1998

Genetic version 4.5
Copyright (c) 1993-2000 CompuLink Ltd.

M protein: protein search using SW model

Search time: 5.78 seconds
(with all parameters)

Search time: 13.4229
Maximum DB size: 200000000
Maximum match: 1000
Listed first 45 summaries

Database: 1: SP_ARCH: 17

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Prod. No. is the number of results predicted by chance. To have a score greater than or equal to the score of the result being returned, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	ID	Accession
1	1.271	99.4	265	10	Q94R26
2	1.271	99.4	265	10	Q94R26
3	1.271	99.4	265	10	Q94R26
4	1.271	99.4	265	10	Q94R26
5	1.271	99.4	265	10	Q94R26
6	1.271	99.4	265	10	Q94R26
7	1.271	99.4	265	10	Q94R26
8	1.271	99.4	265	10	Q94R26
9	1.271	99.4	265	10	Q94R26
10	1.271	99.4	265	10	Q94R26
11	1.271	99.4	265	10	Q94R26
12	1.271	99.4	265	10	Q94R26
13	1.271	99.4	265	10	Q94R26
14	1.271	99.4	265	10	Q94R26
15	1.271	99.4	265	10	Q94R26
16	1.271	99.4	265	10	Q94R26
17	1.271	99.4	265	10	Q94R26
18	1.271	99.4	265	10	Q94R26
19	1.271	99.4	265	10	Q94R26
20	1.271	99.4	265	10	Q94R26
21	1.271	99.4	265	10	Q94R26
22	1.271	99.4	265	10	Q94R26
23	1.271	99.4	265	10	Q94R26
24	1.271	99.4	265	10	Q94R26
25	1.271	99.4	265	10	Q94R26
26	1.271	99.4	265	10	Q94R26
27	1.271	99.4	265	10	Q94R26
28	1.271	99.4	265	10	Q94R26
29	1.271	99.4	265	10	Q94R26
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38	1.271	99.4	265	10	Q94R26
39	1.271	99.4	265	10	Q94R26
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41	1.271	99.4	265	10	Q94R26
42	1.271	99.4	265	10	Q94R26
43	1.271	99.4	265	10	Q94R26
44	1.271	99.4	265	10	Q94R26
45	1.271	99.4	265	10	Q94R26

ALTERNATIVES

Result	Score	Match	Length	ID	Accession
1	1.271	99.4	265	10	Q94R26
2	1.271	99.4	265	10	Q94R26
3	1.271	99.4	265	10	Q94R26
4	1.271	99.4	265	10	Q94R26
5	1.271	99.4	265	10	Q94R26
6	1.271	99.4	265	10	Q94R26
7	1.271	99.4	265	10	Q94R26
8	1.271	99.4	265	10	Q94R26
9	1.271	99.4	265	10	Q94R26
10	1.271	99.4	265	10	Q94R26
11	1.271	99.4	265	10	Q94R26
12	1.271	99.4	265	10	Q94R26
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42	1.271	99.4	265	10	Q94R26
43	1.271	99.4	265	10	Q94R26
44	1.271	99.4	265	10	Q94R26
45	1.271	99.4	265	10	Q94R26

Query Match: 99.4% Score: 1.271; ID: 10; Length: 265;
 Most Local Similarity: 99.4%; ID: 10; Length: 265;
 Most Local Similarity: 99.4%; ID: 10; Length: 265;

УЧАВК 13

ESTGGA 1

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Concentration of inhibitor (mole/l)	Rate of polymerization (mole/l·hr)
0	0.001
0.0001	0.0008
0.0002	0.0006
0.0004	0.0004
0.0006	0.0003
0.0008	0.0002
0.001	0.0001

1. *What is the main purpose of the study?*
2. *What are the research objectives?*
3. *What is the research methodology?*
4. *What are the results of the study?*
5. *What are the conclusions of the study?*

Concentration of inhibitor (mole/l)	Experimental Rate (mole/l·hr)	Calculated Rate (mole/l·hr)
0	0.8	0.8
0.0001	0.6	0.6
0.0002	0.4	0.4
0.0004	0.2	0.2
0.0006	0.15	0.15
0.0008	0.12	0.12
0.001	0.1	0.1

[illegible]

20. *Abstracts of the Proceedings of the 1997 Annual Meeting of the American Psychological Association, Washington, DC, August 1-5, 1997.* *Journal of Consulting and Clinical Psychology*, 65, 1-10.

[illegible]

1. *Introduction*

APPENDIX 1. POLYNOMIALS P_n AND Q_n FOR $n \leq 4$

[illegible]

for polynomials (Kronecker algorithm).

X	$(1, X)$	$4_1, 4_2, 4_3$
$\mathbb{N}_1, \mathbb{N}_2$	$(1, X)$	$4_1, 4_2, 4_3$
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X	$(1, X)$	$4_1, 4_2, 4_3$

SILVERSTEIN A., Astwood J., Charad L., Kistall F.

1. $\text{Pr}(\text{red}) = \frac{1}{2} \log(1 + \sqrt{2})$.

A. Olsen E., Zhang L., Hill P.J., Kishi P.J., Schen A.H., Muddapati V.V., "Identification and characterization of the Pbx-18 dnp of basic"

MC WILLIAMS, JR., 115 E. LEBANON, COOK, FOR HILMAN AND TALBOT, CHICAGO, ILL., TO EXAMINE AND REPORT ON A PROPOSED

known in the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute, there are no entry of records of the

or send an email to info@cs.cmu.edu.

[illegible]

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Al ₂ O ₃ /FeO; $S_{\text{eff}}(\text{mol})$	1.00(1)	1.00(1)	1.00(1)
SiO ₂ /Na ₂ O	1	2K	10^3 [K M] A^2

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1. *Chlorophyll a* (Chl a) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl a is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy.

Polym. Int. J., 2002, Vol. 41, No. 3, pp. 299-304.
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Scoring table: $\text{H}_{\text{max}}/\text{M}_{\text{max}} = 0.5$

Stacy, S. 1995. *Stacy's* 14(272429) 105510025

Total number of hits	Satisfying chosen parameter(s)
minimum 18 seq	1745
maximum 18 seq	1745
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Post	proposition:	Minimum	Match
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fixed M_{ij} is the number of results predicted by class i to have a score greater than or equal to the score of the result being fitted, and is derived by analysis of the total score distribution.

SUMMARY

Result	Score	Quality	Match	Fourth	3B	1D	Result	Score	Quality	Match	Fourth	3B	1D
1	1,400	97.3	265	10	Q9SB60		1	1,400	97.3	265	10	Q9SB60	
2	1,350	97.7	265	10	Q9H342		2	1,350	97.7	265	10	Q9H342	
3	1,242	98.3	263	10	Q9H466		3	1,242	98.3	263	10	Q9H466	
4	1,225	96.9	260	10	Q9H343		4	1,225	96.9	260	10	Q9H343	
5	1,189	95.4	262	10	Q9H344		5	1,189	95.4	262	10	Q9H344	
6	1,019	76.06	276	10	Q9EP99		6	1,019	76.06	276	10	Q9EP99	
7	1,013.5	96.24	305	10	Q9EP99		7	1,013.5	96.24	305	10	Q9EP99	
8	972.5	96.25	305	10	Q9H224		8	972.5	96.25	305	10	Q9H224	
9	949.5	78.3	264	10	Q9H372		9	949.5	78.3	264	10	Q9H372	
10	949.5	78.3	301	10	Q9H399		10	949.5	78.3	301	10	Q9H399	
11	843	96.30	312	10	Q9H341		11	843	96.30	312	10	Q9H341	
12	810.5	45.38	276	10	Q9H349		12	810.5	45.38	276	10	Q9H349	
13	808.5	95.7	276	10	Q9H320		13	808.5	95.7	276	10	Q9H320	
14	837	95.5	312	10	Q9H960		14	837	95.5	312	10	Q9H960	
15	860.5	95.5	276	10	Q9H321		15	860.5	95.5	276	10	Q9H321	
16	824.5	94.5	276	10	Q9H318		16	824.5	94.5	276	10	Q9H318	
17	813.5	93.8	276	10	Q9H367		17	813.5	93.8	276	10	Q9H367	
18	810.5	93.8	240	10	Q9H371		18	810.5	93.8	240	10	Q9H371	
19	809.5	94.5	276	10	Q9H26		19	809.5	94.5	276	10	Q9H26	

20	546.5	42.8	31.3	10	0046.5	004828	lacrimum vit
21	536.5	42.0	179	10	0339.5	004830	lacrimum vit
22	418.5	24.9	138	10	0658.0	004832	lacrimum vit
23	291	22.8	106	10	0658.8	004834	lacrimum vit
24	183	14.3	72.2	14	01308.3	013083	lacrimum vit
25	173	13.5	114.7	2	008784.8	0087848	lacrimum vit
26	172.5	13.5	76.2	5	004040.0	0040400	lacrimum vit
27	172.5	13.5	73.4	5	004041.0	0040410	lacrimum vit
28	161.5	12.6	54.0	9	01303.4	013034	lacrimum vit
29	159	12.5	50.7	13	004616.0	0046160	lacrimum vit
30	159	12.5	67.5	13	004617.0	0046170	lacrimum vit
31	150.5	11.8	76.4	5	005684.0	0056840	lacrimum vit
32	150	11.7	59.5	2	005150.0	0051500	lacrimum vit
33	150	11.7	115.8	2	00727.3	007273	lacrimum vit
34	150	11.7	145.6	2	008136.0	0081360	lacrimum vit
35	146.5	11.5	84.5	5	004716.0	0047160	lacrimum vit
36	145.5	11.4	201.6	5	005203.0	0052030	lacrimum vit
37	144.5	11.3	29.8	2	006041.0	0060410	lacrimum vit
38	144	11.3	346.9	5	006041.0	0060410	lacrimum vit
39	144	11.3	350.2	5	006041.0	0060410	lacrimum vit
40	142.5	11.2	217.8	2	006041.0	0060410	lacrimum vit
41	142	11.1	92.6	5	018501.0	0185010	lacrimum vit
42	142	11.1	263.9	5	026700.0	0267000	lacrimum vit
43	140	11.0	115.6	2	005750.1	0057501	lacrimum vit
44	139	10.9	151.4	5	004010.7	0040107	lacrimum vit
45	137.5	10.8	122.9	5	004010.5	0040105	lacrimum vit

ACKNOWLEDGMENTS

RESULT: 1
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PRELIMINARY: PRI: 26.5 AA

Q95H(0)

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01-MAY-2000	(TEMPHIL)	13,	Last sequence update)
01-MAY-2000	(TEMPHIL)	13,	Last annotation update)
01-MAY-2000	(TEMPHIL)	17,	Last annotation update)

GROUP V ALLERGEN PHIL. P. 5.0204 (FACMENT)
phenyl pralene (common timothy)

1. *Introduction*
 2. *Methodology*
 3. *Results*
 4. *Discussion*
 5. *Conclusion*
 6. *References*
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Viridiplantae: Streptophyta: Embryophyta: Equisetum
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Spermatophyta: Liliopsida: Poales: Poaceae: Poaceae

Chlorophyll

PODGE, Philem.
NORRIS_Tax 110-15957;
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RP SOURCE: FROM N.A.

K. FLEISCH-POLLENZ,
H. HOFFMEYER, published
9249029,
G. J. GILBERT, A. J. SCHMIDT, G.
BECKER, W. H. GILL, AB. H.,
R. L. BUTE, A. J.

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Investigation of different peccolindin isoforms of grass group
*Investigation of different peccolindin isoforms of grass group
RT
allergens (timothy grass pollen) isolated by low-stri laminar cyto

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R1 hybridization--antibody binding capacity and affinity.

R1 Eur. J. Biochem. 247:217-223(1997).

[2] R. N. SIEGENTHAL, FROM N. A. K. P.

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Genital A. of different predominant isoflavors of grass group V

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PR: 2006-09-17
DL: AF069472; AA:25996.1;
EMBL: AF069472; AA:25996.1;
UR: InterPro: IPR001778; PDB: al1et-0b

PR InterPro; PR002914; PolIon_alter4
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Received November 1, 1994; accepted March 1, 1995.

AND THE EFFECTS OF TOLIMETHYLPIPERIDINE AND TOLIMETHYLPIPERIDINE N-oxide ON THE PEA EXPOSED TO VIBRATORY STRESS

[illegible][illegible][illegible]

EX MEDLINE 91268749; PubMed 2051620)
BA WSON E.Y., Zhang L., HUI K.D., KSIL F.T., Nelson A.H., Mohapatra S.S.
Kl "Identification and characterization of the Pox-IX group of fastid
R al viruses of *Kentucky bluegrass* pathogen."
J. Invertebr. Med. Zool. 2(1) (2011).
RE J. INSIDE STRUCTURE POLYMER
I. THE BUILDING BLOCKS OF LIFE FROM AN ALTERNATIVE APPROACH
I SIMILARITY RELATIONS TO THE POX-VIRUS FAMILY OF VIRUSES

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[illegible]

1. **Abstract:** Multiple sequence alignment of human cytochrome P-450 2C9 (CYP2C9) and its orthologs from various species. The alignment was performed using the CLUSTAL W program. The results show that the human CYP2C9 protein is highly conserved among the other species. The alignment was used to construct a phylogenetic tree. The results show that the human CYP2C9 protein is highly conserved among the other species.

2. **Keywords:** CYP2C9, cytochrome P-450, multiple sequence alignment, phylogenetic tree, conserved protein.

3. **Introduction:** Cytochrome P-450 (CYP) is a family of enzymes that are involved in the metabolism of drugs and other xenobiotics. CYP2C9 is one of the most important members of this family. It is responsible for the metabolism of many drugs, including warfarin, phenytoin, and tolbutamide. The CYP2C9 gene is located on chromosome 10 in humans. The CYP2C9 protein is highly conserved among the other species.

4. **Materials and Methods:** The CYP2C9 protein sequences from various species were obtained from the GenBank database. The sequences were aligned using the CLUSTAL W program. The alignment was used to construct a phylogenetic tree using the Neighbor-Joining method.

5. **Results:** The alignment of the CYP2C9 protein sequences from various species showed that the human CYP2C9 protein is highly conserved among the other species. The phylogenetic tree showed that the human CYP2C9 protein is highly conserved among the other species.

6. **Discussion:** The results of this study show that the human CYP2C9 protein is highly conserved among the other species. This suggests that the CYP2C9 protein is highly conserved among the other species.

7. **Conclusion:** The results of this study show that the human CYP2C9 protein is highly conserved among the other species. This suggests that the CYP2C9 protein is highly conserved among the other species.

8. **References:** [1] Smith, J. L., et al. (1999) The CYP2C9 protein is highly conserved among the other species. *Journal of Molecular Biology*, 291, 1-10. [2] Smith, J. L., et al. (1999) The CYP2C9 protein is highly conserved among the other species. *Journal of Molecular Biology*, 291, 1-10.

9. **Abstract:** Multiple sequence alignment of human cytochrome P-450 2C9 (CYP2C9) and its orthologs from various species. The alignment was performed using the CLUSTAL W program. The results show that the human CYP2C9 protein is highly conserved among the other species. The alignment was used to construct a phylogenetic tree. The results show that the human CYP2C9 protein is highly conserved among the other species.

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15. **Conclusion:** The results of this study show that the human CYP2C9 protein is highly conserved among the other species. This suggests that the CYP2C9 protein is highly conserved among the other species.

16. **References:** [1] Smith, J. L., et al. (1999) The CYP2C9 protein is highly conserved among the other species. *Journal of Molecular Biology*, 291, 1-10. [2] Smith, J. L., et al. (1999) The CYP2C9 protein is highly conserved among the other species. *Journal of Molecular Biology*, 291, 1-10.

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result	Score	Query	Match	Length	DB	Prod. No.	Database
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3	1267	us-09-381-903-90	265	10	us-09-381-903-90	3	us-09-381-903-90
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8	1267	us-09-381-903-90	265	10	us-09-381-903-90	8	us-09-381-903-90
9	1267	us-09-381-903-90	265	10	us-09-381-903-90	9	us-09-381-903-90
10	1267	us-09-381-903-90	265	10	us-09-381-903-90	10	us-09-381-903-90
11	1267	us-09-381-903-90	265	10	us-09-381-903-90	11	us-09-381-903-90
12	1267	us-09-381-903-90	265	10	us-09-381-903-90	12	us-09-381-903-90
13	1267	us-09-381-903-90	265	10	us-09-381-903-90	13	us-09-381-903-90
14	1267	us-09-381-903-90	265	10	us-09-381-903-90	14	us-09-381-903-90
15	1267	us-09-381-903-90	265	10	us-09-381-903-90	15	us-09-381-903-90
16	1267	us-09-381-903-90	265	10	us-09-381-903-90	16	us-09-381-903-90
17	1267	us-09-381-903-90	265	10	us-09-381-903-90	17	us-09-381-903-90
18	1267	us-09-381-903-90	265	10	us-09-381-903-90	18	us-09-381-903-90
19	1267	us-09-381-903-90	265	10	us-09-381-903-90	19	us-09-381-903-90

Result	Score	Query	Match	Length	DB	Prod. No.	Database
20	545.5	us-09-381-903-90	42.5	313	10	004828	us-09-381-903-90
21	536.5	us-09-381-903-90	41.8	179	10	039995	us-09-381-903-90
22	437	us-09-381-903-90	26.4	148	10	065864	us-09-381-903-90
23	412	us-09-381-903-90	24.3	106	10	065864	us-09-381-903-90
24	178	us-09-381-903-90	13.9	722	13	014083	us-09-381-903-90
25	166.5	us-09-381-903-90	13.0	734	5	098102	us-09-381-903-90
26	162.5	us-09-381-903-90	12.6	462	13	087848	us-09-381-903-90
27	159.5	us-09-381-903-90	12.4	510	9	093088	us-09-381-903-90
28	155.5	us-09-381-903-90	12.1	845	5	093198	us-09-381-903-90
29	155.5	us-09-381-903-90	12.1	1158	2	005158	us-09-381-903-90
30	154	us-09-381-903-90	12.0	1158	2	007277	us-09-381-903-90
31	154	us-09-381-903-90	12.0	1556	2	098636	us-09-381-903-90
32	153	us-09-381-903-90	11.9	675	13	098111	us-09-381-903-90
33	150	us-09-381-903-90	11.7	764	5	098110	us-09-381-903-90
34	149	us-09-381-903-90	11.6	507	13	013028	us-09-381-903-90
35	149	us-09-381-903-90	11.6	595	2	085684	us-09-381-903-90
36	148.5	us-09-381-903-90	11.6	1156	2	097583	us-09-381-903-90
37	148.5	us-09-381-903-90	11.2	298	2	052089	us-09-381-903-90
38	141.5	us-09-381-903-90	11.0	1229	5	098110	us-09-381-903-90
39	141.5	us-09-381-903-90	11.0	2016	5	098110	us-09-381-903-90
40	141	us-09-381-903-90	11.0	4469	5	098110	us-09-381-903-90
41	141	us-09-381-903-90	11.0	3502	5	098110	us-09-381-903-90
42	140.5	us-09-381-903-90	10.9	2178	2	098110	us-09-381-903-90
43	138.5	us-09-381-903-90	10.8	1440	2	098110	us-09-381-903-90
44	138	us-09-381-903-90	10.7	2639	5	076780	us-09-381-903-90
45	136	us-09-381-903-90	10.6	805	5	001579	us-09-381-903-90

ALTERNATES

Result	Score	Query	Match	Length	DB	Prod. No.	Database
10	us-09-381-903-90	PRELIMINARY:	265	AA			
11	us-09-381-903-90	us-09-381-903-90	265	AA			
12	us-09-381-903-90	us-09-381-903-90	265	AA			
13	us-09-381-903-90	us-09-381-903-90	265	AA			
14	us-09-381-903-90	us-09-381-903-90	265	AA			
15	us-09-381-903-90	us-09-381-903-90	265	AA			
16	us-09-381-903-90	us-09-381-903-90	265	AA			
17	us-09-381-903-90	us-09-381-903-90	265	AA			
18	us-09-381-903-90	us-09-381-903-90	265	AA			
19	us-09-381-903-90	us-09-381-903-90	265	AA			
20	us-09-381-903-90	us-09-381-903-90	265	AA			
21	us-09-381-903-90	us-09-381-903-90	265	AA			
22	us-09-381-903-90	us-09-381-903-90	265	AA			
23	us-09-381-903-90	us-09-381-903-90	265	AA			
24	us-09-381-903-90	us-09-381-903-90	265	AA			
25	us-09-381-903-90	us-09-381-903-90	265	AA			
26	us-09-381-903-90	us-09-381-903-90	265	AA			
27	us-09-381-903-90	us-09-381-903-90	265	AA			
28	us-09-381-903-90	us-09-381-903-90	265	AA			
29	us-09-381-903-90	us-09-381-903-90	265	AA			
30	us-09-381-903-90	us-09-381-903-90	265	AA			
31	us-09-381-903-90	us-09-381-903-90	265	AA			
32	us-09-381-903-90	us-09-381-903-90	265	AA			
33	us-09-381-903-90	us-09-381-903-90	265	AA			
34	us-09-381-903-90	us-09-381-903-90	265	AA			
35	us-09-381-903-90	us-09-381-903-90	265	AA			
36	us-09-381-903-90	us-09-381-903-90	265	AA			
37	us-09-381-903-90	us-09-381-903-90	265	AA			
38	us-09-381-903-90	us-09-381-903-90	265	AA			
39	us-09-381-903-90	us-09-381-903-90	265	AA			
40	us-09-381-903-90	us-09-381-903-90	265	AA			
41	us-09-381-903-90	us-09-381-903-90	265	AA			
42	us-09-381-903-90	us-09-381-903-90	265	AA			
43	us-09-381-903-90	us-09-381-903-90	265	AA			
44	us-09-381-903-90	us-09-381-903-90	265	AA			
45	us-09-381-903-90	us-09-381-903-90	265	AA			

Query Match: 265 AA; 26210 MW; 1644425084419084 080744;
Best local similarity: 98.98; 100.00; 100.00; 100.00;
Matches: 2622; Conservative: 0; Mismatches: 4; Gaps: 0;

[illegible]

373

PK 21 SEP 1998; 98056 0020474;
PK 09 JAN 1998; 98056 0000445.

[illegible][illegible]

[illegible]

Seq	Accession	Length	GC
1	U00001.1	4860	50.81
2	U00002.1	4860	50.81
3	U00003.1	4860	50.81
4	U00004.1	4860	50.81
5	U00005.1	4860	50.81
6	U00006.1	4860	50.81
7	U00007.1	4860	50.81
8	U00008.1	4860	50.81
9	U00009.1	4860	50.81
10	U00010.1	4860	50.81
11	U00011.1	4860	50.81
12	U00012.1	4860	50.81
13	U00013.1	4860	50.81
14	U00014.1	4860	50.81
15	U00015.1	4860	50.81
16	U00016.1	4860	50.81
17	U00017.1	4860	50.81
18	U00018.1	4860	50.81
19	U00019.1	4860	50.81
20	U00020.1	4860	50.81
21	U00021.1	4860	50.81
22	U00022.1	4860	50.81
23	U00023.1	4860	50.81
24	U00024.1	4860	50.81
25	U00025.1	4860	50.81
26	U00026.1	4860	50.81
27	U00027.1	4860	50.81
28	U00028.1	4860	50.81
29	U00029.1	4860	50.81
30	U00030.1	4860	50.81
31	U00031.1	4860	50.81
32	U00032.1	4860	50.81
33	U00033.1	4860	50.81
34	U00034.1	4860	50.81
35	U00035.1	4860	50.81
36	U00036.1	4860	50.81
37	U00037.1	4860	50.81
38	U00038.1	4860	50.81
39	U00039.1	4860	50.81
40	U00040.1	4860	50.81
41	U00041.1	4860	50.81
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80	U00080.1	4860	50.81
81	U00081.1	4860	50.81
82	U00082.1	4860	50.81
83	U00083.1	4860	50.81
84	U00084.1	4860	50.81
85	U00085.1	4860	50.81
86	U00086.1	4860	50.81
87	U00087.1	4860	50.81
88	U00088.1	4860	50.81
89	U00089.1	4860	50.81
90	U00090.1	4860	50.81
91</			

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Gene version 4.5
Copyright (c) 1993 - 2000 Compaq Inc.

OM Protein - protein search, using sw model

Run on: February 13, 2002, 10:58:17 Search Time 98.56 Seconds
(with local hits only)

577,722 hits (with local hits) reported

Hit: 1162

Protein Source: 1 AA

Scoring Table: 100.00, Gap 0.5

Search: 47805, score: 14627.2429, residues: 47805

Number of hits satisfying chosen parameters: 47805

Minimum hit score: 0

Maximum hit score: 20000000

Post-processing: Minimum Match: 08

Maximum Match: 1008
Using List: 45 summaries

Post-class: 17*

1: SP_01644*
2: SP_01644*
3: SP_01644*
4: SP_01644*
5: SP_01644*
6: SP_01644*
7: SP_01644*
8: SP_01644*
9: SP_01644*
10: SP_01644*
11: SP_01644*
12: SP_01644*
13: SP_01644*
14: SP_01644*

Prod. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	OR	ID	Protein
1	1126	96.9	265	10	Q95890	phl1000 prot
2	1126	96.9	265	10	Q95890	phl1000 prot
3	1126	96.8	287	10	Q95890	phl1000 prot
4	1126	96.8	287	10	Q95890	phl1000 prot
5	1102	94.8	293	10	Q95890	phl1000 prot
6	916	78.8	295	10	Q95890	phl1000 prot
7	916	78.4	303	10	Q95890	phl1000 prot
8	841.5	74.2	264	10	Q95890	phl1000 prot
9	841.5	74.2	264	10	Q95890	phl1000 prot
10	841.5	74.2	264	10	Q95890	phl1000 prot
11	747	64.3	312	10	Q95890	phl1000 prot
12	747	64.3	312	10	Q95890	phl1000 prot
13	741.5	63.8	276	10	Q95890	phl1000 prot
14	741.5	63.8	276	10	Q95890	phl1000 prot
15	741.5	63.8	276	10	Q95890	phl1000 prot
16	727.5	62.6	276	10	Q95890	phl1000 prot
17	727.5	62.6	276	10	Q95890	phl1000 prot
18	708.5	61.0	240	10	Q95890	phl1000 prot
19	599.5	51.6	275	10	Q95890	phl1000 prot

20	475.5	40.9	313	10	Q95890	phl1000 prot
21	466.5	40.1	179	10	Q95890	phl1000 prot
22	339.5	29.2	138	10	Q95890	phl1000 prot
23	312	26.9	106	10	Q95890	phl1000 prot
24	174	15.0	722	13	Q95890	phl1000 prot
25	174	15.0	722	13	Q95890	phl1000 prot
26	155.5	13.4	507	13	Q95890	phl1000 prot
27	151.5	13.0	744	5	Q95890	phl1000 prot
28	150.5	13.0	744	5	Q95890	phl1000 prot
29	146	12.6	595	2	Q95890	phl1000 prot
30	145.5	12.5	845	5	Q95890	phl1000 prot
31	145	12.5	4469	5	Q95890	phl1000 prot
32	145	12.5	3502	5	Q95890	phl1000 prot
33	143.5	12.3	675	13	Q95890	phl1000 prot
34	142.5	12.3	1556	2	Q95890	phl1000 prot
35	142	12.2	298	2	Q95890	phl1000 prot
36	139.5	12.0	1201	5	Q95890	phl1000 prot
37	138.5	11.9	764	5	Q95890	phl1000 prot
38	135.5	11.7	540	9	Q95890	phl1000 prot
39	134.5	11.6	2639	5	Q95890	phl1000 prot
40	134	11.5	1346	2	Q95890	phl1000 prot
41	132.5	11.4	846	11	Q95890	phl1000 prot
42	130.5	11.2	2178	2	Q95890	phl1000 prot
43	130.5	11.2	347	12	Q95890	phl1000 prot
44	130	11.2	2016	5	Q95890	phl1000 prot
45	129	11.1	1158	2	Q95890	phl1000 prot

ALPHABETICS

Result	ID	Query Match	Length	OR	ID	Protein
1	Q95890	96.9	265	10	Q95890	phl1000 prot
2	Q95890	96.9	265	10	Q95890	phl1000 prot
3	Q95890	96.8	287	10	Q95890	phl1000 prot
4	Q95890	96.8	287	10	Q95890	phl1000 prot
5	Q95890	94.8	293	10	Q95890	phl1000 prot
6	Q95890	78.8	295	10	Q95890	phl1000 prot
7	Q95890	78.4	303	10	Q95890	phl1000 prot
8	Q95890	74.2	264	10	Q95890	phl1000 prot
9	Q95890	74.2	264	10	Q95890	phl1000 prot
10	Q95890	74.2	264	10	Q95890	phl1000 prot
11	Q95890	64.3	312	10	Q95890	phl1000 prot
12	Q95890	64.3	312	10	Q95890	phl1000 prot
13	Q95890	63.8	276	10	Q95890	phl1000 prot
14	Q95890	63.8	276	10	Q95890	phl1000 prot
15	Q95890	63.8	276	10	Q95890	phl1000 prot
16	Q95890	62.6	276	10	Q95890	phl1000 prot
17	Q95890	62.6	276	10	Q95890	phl1000 prot
18	Q95890	61.0	240	10	Q95890	phl1000 prot
19	Q95890	51.6	275	10	Q95890	phl1000 prot

Query Match: 96.9% Seq ID: 1126, 108, 107, 106, 105, 104, 103, 102, 101, 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80, 79, 78, 77, 76, 75, 74, 73, 72, 71, 70, 69, 68, 67, 66, 65, 64, 63, 62, 61, 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0

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Database version 4.5
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Database version 4.5

February 13, 2002, 10:50:49 - Search time: 0.1 seconds

(with automatic updates)

Pro: 703 Mbit/sec - well updates/sec

US: 9081 903 94

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12 1102 94.8 290 20 AAY250.0
13 1018 87.6 280 20 AAY250.0
14 1018 87.6 280 20 AAY250.0
15 883.5 76.0 301 14 AAY250.0
16 883.5 76.0 301 14 AAY250.0
17 883.5 76.0 301 14 AAY250.0
18 883.5 76.0 301 14 AAY250.0
19 755.5 65.0 312 20 AAY250.0
20 747 64.3 312 20 AAY250.0
21 743.5 64.0 312 20 AAY250.0
22 741 63.8 312 20 AAY250.0
23 741 63.8 312 20 AAY250.0
24 741 63.8 312 20 AAY250.0
25 739.5 63.6 276 20 AAY250.0
26 737.5 63.4 276 20 AAY250.0
27 735 63.2 276 20 AAY250.0
28 734.5 63.2 276 20 AAY250.0
29 734.5 63.2 276 20 AAY250.0
30 734.5 63.2 276 20 AAY250.0
31 734 63.1 276 20 AAY250.0
32 728.5 62.7 286 20 AAY250.0
33 728.5 62.7 286 20 AAY250.0
34 685 59.0 285 20 AAY250.0
35 677.5 58.4 339 20 AAY250.0
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38 670.5 57.7 182 19 AAY250.0
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40 581 50.0 137 19 AAY250.0
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